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Updated analysis of genetic mixing among beluga stocks in the Nunavik marine region and Belcher Islands area: information for population models and harvest allocation

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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ABSTRACT

In the Nunavik marine region and Belcher Islands area, hunters harvest beluga from a mixture of stocks, including the Eastern Hudson Bay (EHB) summer stock that has been considered as Endangered by the COSEWIC since May 2004. The Nunavik Marine Region Wildlife Board developed a 3-year management plan in 2014 establishing a Total Allowable Take (TAT) based on the proportion of EHB beluga harvested seasonally in the different areas of Nunavik. For their part, the community of Sanikiluaq, located in the Belcher Islands (Nunavut), enacted in 2010 a voluntary annual closure of the summer beluga harvest for the period extending from the July 1 to September 30. The start date of the closure period was later changed to July 15 in 2012.

Proportions of EHB belugas in the harvest were estimated through genetic analyses of samples obtained from Inuit hunters. A total of 1,685 samples collected between 1982 and 2015 (including 246 new samples) were used to update the previous results for the different management areas. The analyses indicate that the proportions of EHB beluga in the Hudson Strait harvest were 10.8% in spring and 26.1% in fall which were similar to previous estimates. The number of available samples for north-eastern Hudson Bay in spring and in Ungava Bay during the fall was insufficient for inference. In the Belcher Islands, the proportion of EHB beluga in the spring harvest (April 1- June 30) was estimated to be 1.5%. This proportion increased to 4.4% if spring was extended until July 14. In summer, the updated estimate was 25.6% (July 1 - September 30) and 0% in fall. Besides updating the estimated proportions of the different source populations occurring in the harvest, the additional samples contributed to a decrease in the uncertainty around the estimates.

Mise à jour des analyses génétiques du mélange des stocks de belugas dans la région marine du Nunavik et des Îles Belchers : Information pour les modèles de population et l'allocation de la chasse

RÉSUMÉ

Dans la région marine du Nunavik et le secteur des Îles Belchers, les chasseurs prélèvent des bélugas qui proviennent de plusieurs stocks, incluant celui de l'est de la baie d'Hudson (EBH) qui est considéré comme menacé par le COSEPAC depuis mai 2004. En 2014, le conseil de Gestion des ressources fauniques de la région marine du Nunavik a développé un plan d'aménagement de 3 ans établissant une récolte totale autorisée basée sur la proportion de beluga de l'EBH prélevés par saison dans les différents secteurs du Nunavik. De leur côté, la communauté de Sanikiluaq, localisée dans les Îles Belchers (Nunavut), a décrété en 2010 une fermeture annuelle volontaire de la chasse estivale pour la période s'étendant du 1 juillet au 30 septembre. En 2012, la date de début de la période de fermeture a été repoussée au 15 juillet.

Les proportions de bélugas de l'EBH dans la récolte ont été estimées à l'aide d'analyses génétiques d'échantillons obtenus par les chasseurs Inuits. Un total de 1685 échantillons collectés entre 1982 et 2015 (incluant 246 nouveaux échantillons) ont été utilisés pour mettre à jour les résultats précédents obtenus pour les différentes aires de gestion. Les analyses indiquent que les proportions de bélugas de l'EBH dans la chasse du détroit d'Hudson étaient de 10,8 % au printemps et 26,1 % en automne, ce qui est similaire aux estimés précédents. Le nombre d'échantillons prélevés dans le nord-est de la baie d'Hudson au printemps et dans la baie d'Ungava en automne était insuffisant pour permettre des estimations valides. Dans les Îles Belchers, la proportion de bélugas de l'EBH dans la récolte printanière (1er Avril – 30 Juin) était estimée à 1,5 %. Cette proportion augmentait à 4,4 % si la période printanière était étendue jusqu'au 14 juillet. En été, elle était estimée à 25,6 % et à 0 % en automne. En plus de mettre à jour les estimés des proportions des différentes populations sources présentes dans la récolte, l'ajout de nouveaux échantillons contribue à diminuer l'incertitude autour de ces estimés.

INTRODUCTION

The beluga (*Delphinapterus leucas*) is a toothed whale with pan-Arctic distribution extending into the Hudson Bay complex in sub-Arctic eastern Canada (Richard and Pike 1993). Subsistence hunting of beluga by Nunavik Inuit (northern Quebec) is directed towards a migratory population that winters in Hudson Strait and the Labrador Sea. Photo-identification, satellite telemetry and genetic studies have shown that beluga exhibit strong seasonal site fidelity to specific congregation areas during summer (Caron and Smith 1990; de March and Postma 2003, Lewis et al. 2009). Despite interbreeding on wintering grounds (Turgeon et al. 2012), cultural conservatism of maternally-transmitted migration routes seems to prevent substantial exchange between these summering aggregations (Colbeck et al. 2012), thus making beluga vulnerable to local extirpation (COSEWIC 2004).This cumulative evidence has led to the current use of discrete summering stocks as management units (e.g., Smith and Hammill 1986, Richard 2010).

Most summer aggregations of beluga across the Canadian Arctic are genetically differentiated by mtDNA analyses (Brennin et al. 1997; Brown Gladden et al. 1999; de March and Postma 2003). In eastern Canada, studies have clearly demonstrated that the eastern Hudson Bay (EHB) stock is differentiated from the adjacent Western Hudson Bay (WHB) stock, although both belong to the same breeding population (Turgeon et al. 2012). The EHB stock was depleted by intensive commercial hunting in the nineteenth century (Reeves and Mitchell 1987). It was designated by COSEWIC as Threatened in April 1988, but then downlisted to Endangered in May 2004.

With the signing of the Nunavik Inuit Land Claim Agreement (Anonymous 2008), the Nunavik Marine Region Wildlife Board (NMRWB) became the main instrument of wildlife management for the Nunavik Marine Region (NMR). The objectives of the NMRWB are to establish wildlife management systems that reflect Nunavik Inuit harvesting rights, while being governed by the principles of conservation (NILCA s. 5.1.3 (a) and (c)). Given existing conservation concerns for EHB beluga, the NMRWB proposed a 3-year management plan in 2014 that was approved and implemented by DFO. The plan established a Total Allowable Take (TAT) for the EHB beluga stock.

Estimating the number of harvested EHB beluga is complex. A common migratory corridor in north-eastern Hudson Bay, Hudson Strait and Ungava Bay, is shared by EHB beluga and beluga from other summer stocks. There is no way for hunters to distinguish among these migratory stocks. Genetic studies indicate that the proportion of each stock in the harvest varies spatially and seasonally (de March and Postma 2003; Turgeon et al. 2012). Therefore, genetic analyses of skin samples provided by hunters have been used to estimate the proportions of EHB beluga in seasonal harvests from different areas to inform population models and management schemes (Doniol-Valcroze et al. 2016).

Belugas are also observed around the Belcher Islands, located within the Nunavut Settlement Area and are harvested by hunters from the community of Sanikiluaq. Their relationship to other summer stocks is unclear, but they are not currently considered a distinct management stock and are not surveyed separately during Nunavik beluga censuses (Hammill et al. 2004). Satellite telemetry studies have shown that EHB beluga may be vulnerable to being harvested in the Belcher Islands, especially in summer and fall (Doniol-Valcroze and Hammill 2012), but previous genetic analyses suggest that few EHB beluga are taken during Sanikiluaq spring and fall hunts (Doniol-Valcroze et al. 2016). There is no formal management plan or legal harvest restriction for Nunavut hunters living in the Belcher Islands. However, the community of Sanikiluaq has enacted beluga hunting rules including, since 2010, a voluntary annual closure

of the summer beluga harvest in the Belcher Islands (between July 1 and September 30) as a conservation measure in support of EHB beluga recovery. In 2012, the start of the voluntary harvest closure start date was changed to July 15.

This document's main aim is to update the analysis of genetic mixing among beluga stocks occurring in the Nunavik marine region and the Belcher Islands area with the new information acquired in 2014 and 2015 in order to refine our estimates of the proportion of EHB beluga harvested by Nunavik communities and the Nunavut community of Sanikiluaq.

MATERIALS AND METHODS

BIOLOGICAL SAMPLING AND GENETIC CHARACTERIZATION

Beluga tissue samples were obtained from Hudson Bay and surrouncing areas. A few samples were collected by DFO during deployment of satellite transmitters, but the vast majority of samples were obtained from Nunavik and Nunavut hunters during harvest. In Nunavik, a sampling program was initiated in collaboration with Makivik Corporation in the 1980's. A similar program is in place in Sanikiluaq, as well as western Hudson Bay communities. Hunters participate in the program on a voluntary basis and receive financial compensation for providing samples.

Samples from the hunt were collected on-site and provided to DFO along with information such as date and location. Although the availability and reliability of this information has increased through time, it is missing in some cases. Moreover, hunters from some communities in Hudson Bay and Ungava Bay travel to other areas (mostly Hudson Strait) to hunt beluga. It is therefore crucial to assign samples to the correct hunting area. Reports from hunters and Uumajuit wardens were used to locate the exact site where each beluga was killed for both new and previous samples. When hunting location could not be determined with confidence, samples were removed from the analysis.

DNA extraction, molecular determination of sex and sequencing of a portion of the mitochondrial DNA D-loop region were performed using methods described in de March and Postma (2003) and in Postma et al. (2012). DNA sequences were aligned, edited, and haplotype identified using SeqScape (Applied Biosystems, Thermofisher Scientific).

GENETIC MIXTURE ANALYSIS

This genetic stock identification analysis estimates the proportion of individuals belonging to the different source stocks (i.e. distinct summer stocks) in the composition of the population hunted in different areas and periods. Mitochondrial DNA (mtDNA) haplotypes were used as markers allowing differentiation among the source stocks. Samples used in our analysis include data considered in Doniol-Valcroze et al. (2016) covering 1982 to 2013, plus new samples collected between 2013 and 2015. Moreover, the continual update of techniques and equipment used for genetic analysis allowed for the reevaluation of some samples and the correction of some errors that occurred in the previous version of the dataset.

Following Doniol-Valcroze et al. (2016), two source stocks were defined by samples taken in July and August in summering areas of WHB and EHB (de March et al. 2002; de March and Postma 2003; COSEWIC 2004). Taking into account current management units, four areas where there is mixing of source populations were considered along the common seasonal migratory corridor (Fig. 1): northeastern Hudson Bay (NEHB), southern Hudson Strait (HS), Ungava Bay (UNG) and Sanikiluaq (SAN).

For NEHB, HS and UNG, two hunting seasons were examined separately: "Spring" (February 1 to August 31) and "Fall" (September 1 to January 31). A more detailed analysis was conducted with samples coming from the Sanikiluaq area. Since 2010, the spring hunt is bounded by voluntary closure dates, first from April 1 to June 30 until 2012, then from April1 to July 14 post-2012. We examined these two definitions of the spring hunt season as "Spring and "Spring extended", respectively. The "Summer" period included all July-August samples. "Fall" (September – November) and "Winter" (December – March) periods were examined separately because most of the winter samples come from ice entrapment events, at a time when EHB beluga are believed to have left the area.

Genetic mixture analyses were performed using SPAM version 3.7b (Debevec et al. 2000, Alaska Department of Fish and Game 2003, Doniol-Valcroze et al. 2016).

"Sampling zeros" problematic

A preliminary analysis of the dataset indicated that some haplotypes found in the mixed stock migratory sample did not occur in the baseline summer stock samples used to describe the two source populations we considered (i.e. WHB or EHB). This can occur with a small baseline sample size, and/or when the missing haplotypes are rare and thus unlikely to be sampled in the population, and/or when baselines do not include all the potential source populations. Unfortunately, this can potentially result in biases in the mixture estimates. However, SPAM v3.7b proposes two Bayesian mixture analysis methods that can circumvent this problem. In both the Rannala-Mountain (Rannala and Mountain 1997) and Pella-Masuda (Pella and Masuda 2001) models, posterior means of haplotype frequencies are positive, thus implying that the absence of a haplotype from the baseline samples is caused by its rarity and not by the fact that it is non-existent. The Rannala-Mountain method supposes that all sources potentially contributing to the mixed population are known, while the Pella-Masuda model allows for the possible occurrence of an unknown population. Considering that some uncertainties persist about the stocks contributing to the migratory whales that are hunted (Turgeon et al. 2012), we decided to use the Pella-Masuda approach. We first tested the impact of using this method in applying it on the dataset used by Doniol-Valcroze et al. (2016) and checking differences with their results. Then, the Pella-Masuda method was applied to the revised and updated dataset covering 1982 to 2015.

Effect of clustering of samples within hunting events

As mentioned in Doniol-Valcroze et al. (2016), the fact that beluga travel in social groups of related individuals (Colbeck et al. 2012) can create a bias in the frequency of occurrence of some haplotypes as members of the same group have a high likelihood of sharing the same haplotype. As a result, samples of individuals hunted during the same hunting event are correlated. While SPAM gives measures of error considering each sample as independent, we took into account the autocorrelation between samples in computing standard errors using a leave-one-out jackknife resampling procedure, i.e. by removing at each iteration all samples from a definite event. Because samples were not identified to specific hunting events, we considered individuals hunted on the same date as being hunted during the same event.

RESULTS

HAPLOTYPES

The updated dataset includes 1,807 samples for which the mitochondrial DNA haplotype was identified. From those, 122 could not be considered due to missing information on hunting date,

limiting the sample used in this study to 1,685 individuals (vs. 1,439 in the previous assessment; corrected from Doniol-Valcroze et al. 2016). No new samples were available from the WHB source population (132 individuals) but 10 were added to the EHB source sample totaling 195 individuals. A total of 1,064 samples were available from the Nunavik mixed hunt areas (Table 1, 22 from NEHB, 964 from HS and 78 from UNG) and 426 from the Sanikiluaq. From those, 71 samples were added in 2014 (1 from NEHB, 53 from HS, and 17 from Sanikiluaq) and 121 in 2015 (50 from HS, 11 from UNG, and 60 from Sanikiluaq). Furthermore, hunting dates were located for some older samples, which add 5 samples to HS and 40 to Sanikiluaq.

GENETIC MIXTURE ANALYSIS

Methods comparisons

The use of the Pella-Masuda model on the same dataset used by Doniol-Valcroze et al. (2016) resulted in a mean decrease of 0.6% (range -1.1 – 0.1) in the proportion of hunted animals assigned to EHB population (Table 2 vs. Table 3) and a corresponding increase in the proportion assigned to the WHB population. The proportion of animals that could not be assigned to one population or the other (i.e., Unknown source) did not change with the method used (except for the Sanikiluaq winter harvest with a 0.1% increase). Results obtained with the Pella-Masuda model also generally show a slight increase in error around the proportion estimates (mean increase of 0.6% of the 95%CI ranges (range -0.2 – 1.6)).

Updated dataset

The haplotype frequencies observed in the harvest samples from the Nunavik mixed hunt areas and Sanikiluaq are shown in Figure 2 and 3 respectively.

In the Nunavik spring hunt, the proportion of EHB beluga was estimated to be 10.8% (CV 0.18, N=611, Table 4) for Hudson Strait, and 8.4% (CV 0.6, N=75) for Ungava Bay. In fall, 26.1% (CV=0.12, N=352) and 30.2% (CV=0.4, N=20) of the animals hunted respectively in the Hudson Strait and in the Northeast Hudson Bay were attributed to EHB. The proportion of the latter in the Ungava Bay summer hunt was estimated to be 3.1% (CV=1.14, N=51).

The proportion of EHB animals harvested in the spring in the northeastern Hudson Bay and in fall in Ungava Bay were not estimated due to the small number of samples available (spring NEHB N=2, fall UNG N=3, Table 4).

The proportion of EHB beluga in the Sanikiluaq spring harvest, was estimated to be 1.5% (CV=1.07, N=297, Table 4) for the period April 1- June 30 and 4.4% (CV=0.43, N=320) for the period April 1 – July 14. In summer, the estimated proportion of EHB beluga increased to 25.6% (CV=0.37, N=31) while it is considered nill (0.0%, N=42) in fall. The estimated proportion of EHB beluga in the winter samples was 36.6% (CV=0.21, N=56).

Over all hunting seasons and areas, the proportion of the harvest attributed to unknown population(s) ranged from about 3% (Hudston Strait and Sanikiluaq fall hunts) to 32% (Sanikiluaq winter hunt), revealing the potential occurrence of other source populations not incorporated into this analysis.

The jackknife procedure using a leave-one-date-out in order to evaluate among event variability, resulted generally in an increased value of the error (CV samples vs CV events, Table 3) around the proportion estimates. Confidence intervals provided in Table 4 (i.e., 95%CI) were calculated using error obtained from the jackknife procedure.

DISCUSSION

This update of the genetic mixing among Nunavik beluga summer stocks includes additional samples harvested in 2014 and 2015 (N=80 in 2014, N=133 in 2015) as well as samples from previous years that were not included in the previous analysis due to missing information (e.g. missing hunting date). Moreover, some data included in the dataset used by Doniol-Valcroze et al. (2016) were modified when samples were re-sequenced using updated methods.

Preliminary analysis of the dataset detected haplotypes in the hunted sample that had not been identified in the source stocks. To avoid the potential bias in the estimates caused by this situation (Smouse et al. 1990), we used a Bayesian method (Pella and Masuda 2001) to consider the baseline information (i.e. the information on haplotype frequencies in the source stocks) in the genetic mixture analysis. Apart from this, the analysis was identical to Doniol-Valcroze et al. (2016). We assessed the impact of this modification in re-analysing the dataset used by Doniol-Valcroze et al. (2016). The proportion estimates generally changed by 1% or less and increased the error around the estimates slightly. We decided to apply the modification of the analysis to the updated dataset.

The estimated proportion of EHB beluga in the Hudson Bay spring harvest is 10.8% (95%CI 7.1 – 15.2) which is slightly lower (but not significantly different) than the estimated proportion of 11.7 (95%CI 8.0 – 16.4, Table 4) in Doniol-Valcroze et al. (2016). Most of the decrease in the estimated proportion of EHB beluga could be attributed to the application of the Pella-Masuda model for the baselines, because our reanalysis of the dataset used in the previous study (Table 3, i.e. using data from 1982-2013) already estimated this proportion to be 10.7% (95%CI 6.7 – 15.6). However, the addition of new samples increased our confidence in results with the 95%CI narrowing slightly from 6.7-15.6 to 7.1-15.2 (Tables 3, 4). In the fall harvest, the proportion of EHB beluga is slightly higher than in the previous update, having changed from an estimated 23.6% (95%CI 17.9 – 29.9, Table 2), to 26.1% (95%CI 19.3-33.6, Table 4).

The sample size in spring northeastern Hudson Bay and fall Ungava Bay harvests remain too small (N= 2 and 3, respectively, no new data added) precluding any conclusion for those regions/periods. However, the spring Ungava Bay dataset, benefited from 11 new samples for a total of 75. The proportion of EHB beluga in this harvest remained essentially the same with an estimated 8.8% (95%CI 1.9-20.3) in the previous assessment and a current estimate of 8.4% (95%CI 0.9-23, Table 4). The sample size of the northeastern Hudson Bay area remains low for the fall period (N=20) and therefore the estimated proportions in that harvest should be used with caution.

The Sanikiluaq dataset was increased by 17 new samples in 2014 and 60 in 2015. Moreover, thanks to meticulous cross-checks among various databases several dates of hunting were recovered for samples obtained in previous years (N= 40), allowing for their integration into the genetic analysis. The sample size of the Sanikiluaq spring hunt increased to 297 (vs. 191 in the previous study). The proportion of EHB beluga in the spring hunt (April 1 – June 30) was estimated to be 1.5% compared to 2.8% in the previous exercise. Moreover, the increased sample size reduced the uncertainty around the estimates as shown by a 95%CI of 0 – 5.7 (vs. 95%CI 0.3 - 7.7). For the extended spring period (April 1 – July 14), the estimated proportion of EHB beluga in the previous analysis was 6.5% (95%CI 2.0 – 13.3), but has now declined slightly to 4.4% (95%CI = 1.1 – 9.9). The estimated proportion of EHB animals in the summer hunt also declined from 30.6% (95%CI 5.9-64.6) to an estimated 25.6% (95%CI 5.2 – 55.1). The analysis of fall samples suggests that no EHB beluga (0%) were taken in that hunt. No new skin samples were added to the analysis of the winter hunt, but 10 samples were added to the dataset constituting the EHB baseline source population. As a result, the estimated proportion of EHB animals taken in the winter declined from 39.8% (95% CI 14.8-68.2) to 36.6% (95%CI 10.5

– 68.2). The addition of 10 samples to the EHB baseline dataset likely better represents the genetic diversity of this source stock and reduced slightly the uncertainty around the estimates.

The addition of new samples has improved our understanding of mixing of the EHB and WHB stocks during the hunting period. Besides updating the estimated proportions of the different source populations occurring in the harvest, the additional samples contributed to a decrease in the uncertainty around the estimates. The continuity of the different sampling programs providing genetic information from harvested belugas is crucial to support the best management practices ensuring a sustainable maintenance of beluga stocks in Nunavik and adjacent waters. Similarly, the regular update of this genetic analysis ensures that the best information is incorporated into the population model used to provide harvest advice.

Some uncertainties persist about the stocks contributing to the migratory whales that are hunted (Turgeon et al. 2012; this study). Further studies involving analysis using more detailed genetic information and information of animal movement acquired by telemetry (e.g. GPS or ARGOS tags) are needed to identify the various migration fluxes occurring in the Nunavik marine region and the Belcher island area.

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REFERENCES CITED

Alaska Department of Fish and Game. 2003. SPAM Version 3.7: Statistics Program for Analyzing Mixtures. Alaska Department of Fish and Game, Commercial Fisheries Division, Gene Conservation Lab.

Anonymous. 2008. Nunavik Inuit Land Claims Agreement. Pages 22-53. Ottawa, Canada.

Brennin, R., Murray, B.W., Friesen, M.K., Maiers, L.D., Clayton, J.W. and White, B.N. 1997. Population genetic structure of beluga whales (*Delphinapterus leucas*): Mitochondrial DNA sequence variation within and among North American populations. Can. J. Zool. 75: 795-802.

Brown Gladden, J.G., Ferguson, M.M., Friesen, M.K. and Clayton, J.W. 1999. Population structure of North American beluga whales (*Delphinapterus leucas*) based on nuclear DNA microsatellite variation and contrasted with the population structure revealed by mtDNA variation. Mol. Ecol. 8: 347-3 63

Caron, L.M.J. and Smith, T.G. 1990. Philopatry and site tenacity of belugas, *Delphinapterus leucas*, hunted by the inuit at the Nastapoka estuary, eastern Hudson Bay. In Smith, T.G., D.J. St.Aubin, and J.R. Geraci (ed.). Advances in research on the beluga whale, *Delphinapterus leucas*. Can. Bull. Fish. Aquat. Sci. 224: 69-79.

Colbeck, G., Duchesne, P., Postma, L.D., Lesage, V., Hammill, M. and Turgeon, J. 2012. Groups of related belugas (*Delphinapterus leucas*) travel together during their seasonal migrations in and around Hudson Bay. Proc. R. Soc. B-Biol. Sci. 280 doi: 10.1098/rspb.2012.2552.

COSEWIC. 2004. COSEWIC assessment and update status report on the beluga whale *Delphinapterus leucas* in Canada. Committee on the Status of Endangered Wildlife in Canada. Ottawa. ix + 70 pp.

de March, B.G.E., Maiers, L.D. and Friesen, M.K. 2002. An overview of genetic relationships of Canadian and adjacent populations of belugas (*Delphinapterus leucas*) with emphasis on Baffin Bay and Canadian eastern Arctic populations. NAMMCO Sci. Publ.4: 17-38.

de March, B.G.E. and Postma, L.D. 2003. Molecular genetic stock discrimination of belugas (*Delphinapterus leucas*) hunted in eastern Hudson Bay, Northern Quebec, Hudson Strait, and Sanikiluaq (Belcher Islands), Canada, and comparisons to adjacent populations. Arctic 56:111-124.

Debevec, E. M., Gates, R. B., Masuda, M., Pella, J., Reynolds, J., and Seeb, L. W. 2000. SPAM (Version 3.2): Statistics Program for Analyzing Mixtures. J. Hered. 91 (6):509-510.

Doniol-Valcroze, T. and Hammill, M. O. 2012. Harvest advice for beluga in the Belcher, King George, and Sleeper Islands in relation to the eastern Hudson Bay stock. DFO Can. Sci. Advis. Sec. Res. Doc. 2011/125. iv + 8 p.

Doniol-Valcroze, T., Hammill, M.O., Turgeon, S. and Postma, L.D. 2016. Updated analysis of genetic mixing among Nunavik beluga summer stocks to inform population models and harvest allocation. DFO Can. Sci. Advis. Sec. Res. Doc. 2016/008. iv + 13 p.

Hammill, M.O., Lesage, V. Gosselin , J.-F. Bourdages, H. de March, B. G.E. and Kingsley, M.C.S. 2004. Changes in abundance of northern Quebec (Nunavik) beluga. Arctic 57:183-195.

Lewis, A.E., Hammill, M., Power, M., Doidge, D.W. and Lesage, V. 2009. Movement and Aggregation of Eastern Hudson Bay Beluga Whales (*Delphinapterus leucas*): A Comparison of Patterns Found through Satellite Telemetry and Nunavik Traditional Ecological Knowledge. Arctic 62: 13-24.

Pella, J, and Masuda, M. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fish. Bull. 99:151-167

Postma, L.D., Petersen, S.D., Turgeon, J., Hammill, M.O., Lesage, V., and Doniol-Valcroze, T. 2012. Beluga whales in James Bay: a separate entity from eastern Hudson Bay belugas? DFO Can. Sci. Advis. Sec. Res. Doc. 2012/074. iii + 23 p.

Rannala, B., and Mountain, J. L. 1997. Detecting immigration by using multilocus genotypes. Proc. Natl. Acad. Sci. USA 94: 9197-9201.

Reeves, R.R. and Mitchell, E.D. 1987. History of white whale (*Delphinapterus leucas*) exploitation in eastern Hudson Bay and James Bay. Can. Spec. Publ. Fish. Aquat. Sci. 95. 45p.

Richard, P.R. 2010. Stock definition of belugas and narwhals in Nunavut. DFO Can. Sci. Advis. Sec. Res. Doc. 2010/022. iv + 14.

Richard, P.R. and Pike, D.G. 1993. Small whale co-management in the eastern Canadian Arctic: a case history and analysis. Arctic 46:138–143.

Smith, T.G. and Hammill, M.O. 1986. Population estimates of white whale, *Delphinapterus leucas*, in James Bay, Eastern Hudson Bay and Ungava Bay. Can. J. Fish. Aquat. Sci. 43: 1982-1987.

Smouse, P. E., Waples, R. S., and Tworek, J. A. 1990. A genetic stock-mixture analysis for use with incomplete source population data. Can. J. Fish. Aquat. Sci.47:620–634.

Turgeon, J., Duchesne, P., Colbeck, G.J.C., Postma, L. and Hammill, M.O. 2012. Spatiotemporal segregation among summer stocks of beluga (*Delphinapterus leucas*) despite nuclear gene flow: implication for an endangered population in eastern Hudson Bay (Canada). Conserv. Gen. 13:419-433.

TABLES

Table 1. Number of samples available for each management area and each hunting season, for the 1982-2015 period.

Area	Spring		Summer			Fall			Winter		
	May	June	July	Aug	Sept	Oct	Nov	Dec	Jan	Feb	March
Hudson Strait	3	482	114	12	27	217	108	1	0	0	0
Ungava Bay	0	24	45	6	0	2	0	1	0	0	0
NE Hudson Bay	2	0	0	0	1	19	0	0	0	0	0
Sanikiluaq	81	216	28	3	18	22	2	37	0	12	7

Area	Spring		Summer			Fall			Winter		
	May	June	July 1-14	July 15-31	Aug	Sept	Oct	Nov	Dec	Jan	Feb	March
Sanikiluaq extended spring	81	216	23	5	3	18	22	2	37	0	12	7

Table 2. Results of the genetic mixture analysis from Doniol-Valcroze et al. 2016. Proportions of beluga (%) from each source stock in the harvest of Nunavik hunt areas (upper part) and Sanikiluaq harvest (lower part), based on genetic mixture analysis of mtDNA haplotype distribution. Software used: SPAM (Debevec et al. 2000). N samples: number of individual samples; N events: number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; 95%CI: 95% confidence interval based on variance among hunting events; CV: coefficients of variation based on individual samples / hunting events. ND: not determined (small sample size).

	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples / events)	% Unknown
Spring (Feb 1 - Aug 31)									
Hudson Strait	539	252	82.2	76.9 - 86.6	0.02/0.03	11.7	8.0 - 16.4	0.17/0.19	6.1
NE Hudson	2	1	ND			ND	-	-	-
Ungava Bay	64	42	83.4	72.5 - 92.0	0.06/0.06	8.8	1.9 - 20.2	0.54/0.55	7.8
Fall (Sept 1 - Jan 31)									
Hudson Strait	318	131	73.3	65.8 - 80.2	0.04/0.05	23.6	17.0 - 30.9	0.13/0.15	3.2
NE Hudson	19	7	56.3	28.3 – 82.2	0.23/0.25	33.2	14.9 – 54.7	0.38/0.31	10.5
Ungava Bay	3	3	ND	-	-	ND	-	-	ND

Sanikiluaq

Season	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples)	% Unknown
Spring (April 1 - June 30)	191	81	78.9	70.7 – 86.1	0.03/0.05	2.8	0.3 - 7.7	0.64/0.7	18.3
Extended spring (April 1 - July 14	212	92	76.5	68.6 - 83.9	0.03/0.05	6.6	2.0 - 13.3	0.36/0.45	17.0
Summer (July 1 - August 31)	29	16	55.7	23.8 – 85.1	0.19/0.29	30.6	5.9 - 64.6	0.35/0.51	13.8
Fall (September 1 - November 30	33	24	97.0	89.2 - 99.9	0.01/0.03	0.0	-	-	3.0
Winter (December 1 - March 31)	56	6	28.1	7.8 – 55.1	0.28/0.44	39.8	14.8 - 68.2	0.20/0.35	32.1

Table 3. Results of the genetic mixture analysis using the Pella-Masuda model for the baselines and the same dataset as from Doniol-Valcroze et al. (2016). Proportions of beluga (%) from each source stock in the harvest of Nunavik hunt areas (upper part) and Sanikiluaq harvest (lower part), based on genetic mixture analysis of mtDNA haplotype distribution. Software used: SPAM (Debevec et al. 2000). N samples: number of individual samples; N events: number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; 95%CI: 95% confidence interval based on variance among hunting events; CV: coefficients of variation based on individual samples / hunting events. ND: not determined (small sample size).

	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples / events)	% Unknown
Spring (Feb 1 - Aug 31)									
Hudson Strait	539	252	83.2	77.8 - 87.9	0.02/0.03	10.7	6.7 - 15.6	0.19/0.21	6.1
NE Hudson	2	1	ND			ND	-	-	-
Ungava Bay	64	42	84.4	72.4 - 93.5	0.06/0.06	7.8	1.1 - 20.2	0.62/0.65	7.8
Fall (Sept 1 - Jan 31)									
Hudson Strait	318	131	74.0	66.3 - 81	0.04/0.05	22.8	16.2 - 30.2	0.13/0.16	3.2
NE Hudson	19	7	56.7	28.2 - 82.9	0.23/0.25	32.8	13.9 - 55.3	0.4/0.33	10.5
Ungava Bay	3	3	ND	-	-	ND	-	-	ND

Sanikiluaq

Season	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples / events)	% Unknown
Spring (April 1 - June 30)	191	81	80.0	72.1 - 86.9	0.03/0.05	1.7	0 - 7.2	1.07/1.17	18.3
Extended spring (April 1 - July 14)	212	92	77.4	68.7 - 85	0.03/0.05	5.6	1.2 - 13	0.43/0.55	17.0
Summer (July 1 - August 31)	29	16	56.1	23.9 - 85.6	0.2/0.29	30.1	5.4 - 64.6	0.36/0.52	13.8
Fall (September 1 - November 30)	33	24	97.0	88.8 - 99.9	0.01/0.03	0.0	-	-	3.0
Winter (December 1 - March 31)	56	6	28.0	7.5 - 55.5	0.29/0.45	39.9	14.3 - 69	0.21/0.36	32.2

Table 4. Results of the genetic mixture analysis using the Pella-Masuda model for the baselines and the updated dataset (1982-2015). Proportions of beluga (%) from each source stock in the harvest of Nunavik hunt areas (upper part) and Sanikiluaq harvest (lower part), based on genetic mixture analysis of mtDNA haplotype distribution. Software used: SPAM (Debevec et al. 2000). N samples: number of individual samples; N events: number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; 95%CI: 95% confidence interval based on variance among hunting events; CV: coefficients of variation based on individual samples / hunting events. ND: not determined (small sample size).

	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples / events)	% Unknown
Spring (Feb 1 - Aug 31)									
Hudson Strait	611	278	83.1	78.3 - 87.4	0.02/0.03	10.8	7.1 - 15.2	0.18/0.19	6.1
NE Hudson	2	1	ND			ND	-	-	-
Ungava Bay	75	49	82.3	68.1 – 92.9	0.06/0.08	8.4	0.9 - 23	0.60/0.70	9.3
Fall (Sept 1 - Jan 31)									
Hudson Strait	352	146	71.1	63.4 - 78.1	0.04/0.05	26.1	19.3 - 33.6	0.12/0.14	2.8
NE Hudson	20	8	59.8	31.1 - 85.2	0.21/0.24	30.2	12.1 - 52.3	0.40/0.35	10.0
Ungava Bay	3	3	ND	-	-	ND	-	-	ND

Sanikiluaq

Season	N samples	N events	% WHB	95% CI	(CV samples / events)	% EHB	95% CI	(CV samples / events)	% Unknown
Spring (April 1 - June 30)	297	107	77.3	70.0 - 83.9	0.02/0.05	1.5	0.0 - 5.7	1.07/1.08	21.2
Extended spring (April 1 - July 14)	320	120	75.6	67.9 - 82.5	0.03/0.05	4.4	1.1 - 9.9	0.43/0.52	20.0
Summer (July 1 - August 31)	31	18	61.5	33.6 - 85.7	0.16/0.22	25.6	5.2 - 55.1	0.37/0.51	12.9
Fall (September 1 - November 30)	42	28	97.6	91.3 - 99.9	0.00/0.02	0.0	-	-	2.4
Winter (December 1 - March 31)	56	7	31.3	7.4 – 63.0	0.24/0.47	36.6	10.5 - 68.2	0.21/0.41	32.1

FIGURES

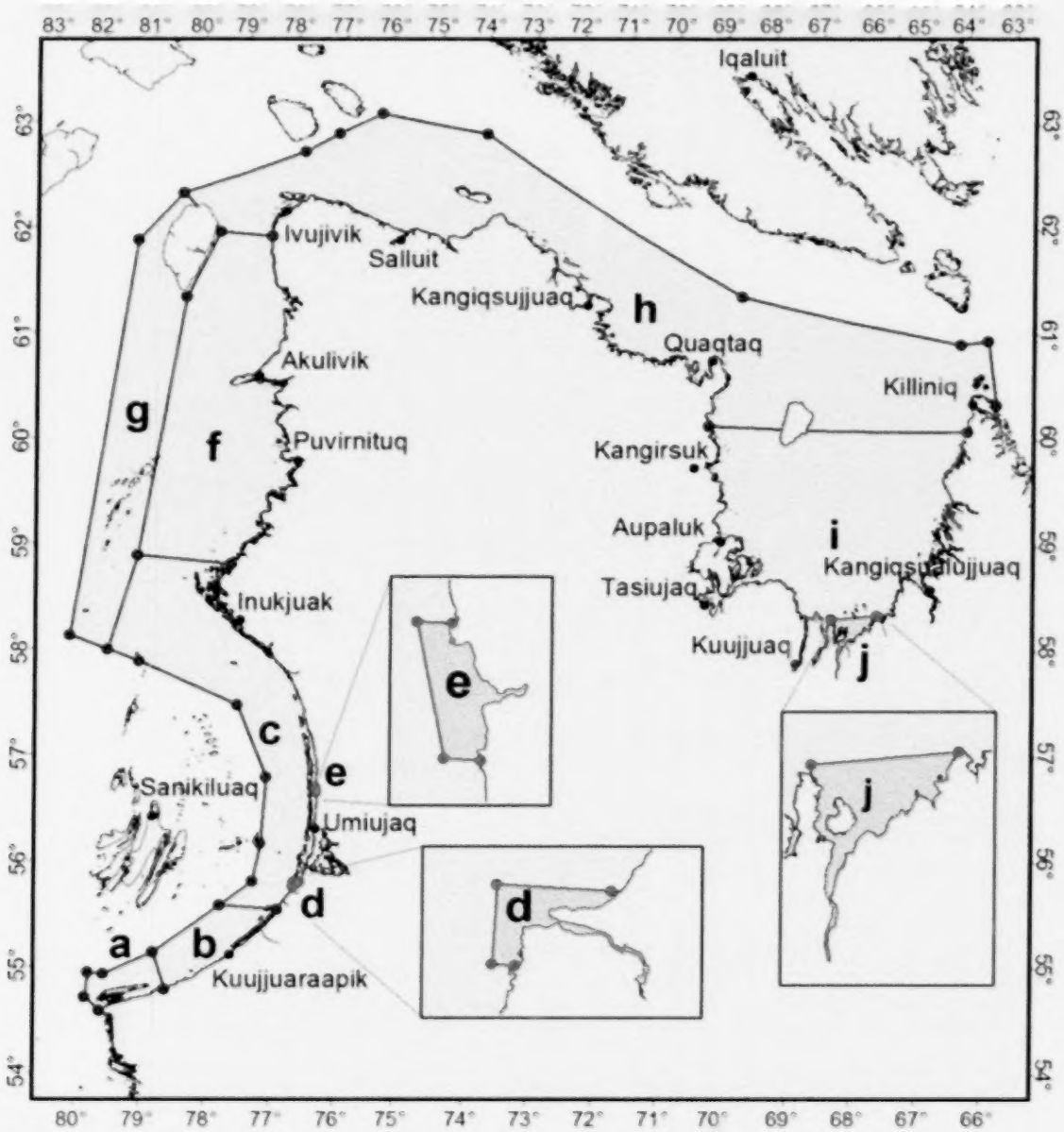

Figure 1. Map of Nunavik communities and management areas for Nunavik beluga (source: Nunavik Marine Region Wildlife Board). In our analysis, the Hudson Strait mixed hunt corresponds to area "h", Ungava Bay to area "i", northeast Hudson Bay to area "f", and the eastern Hudson Bay arc to areas "b", "c", "d" and "e".

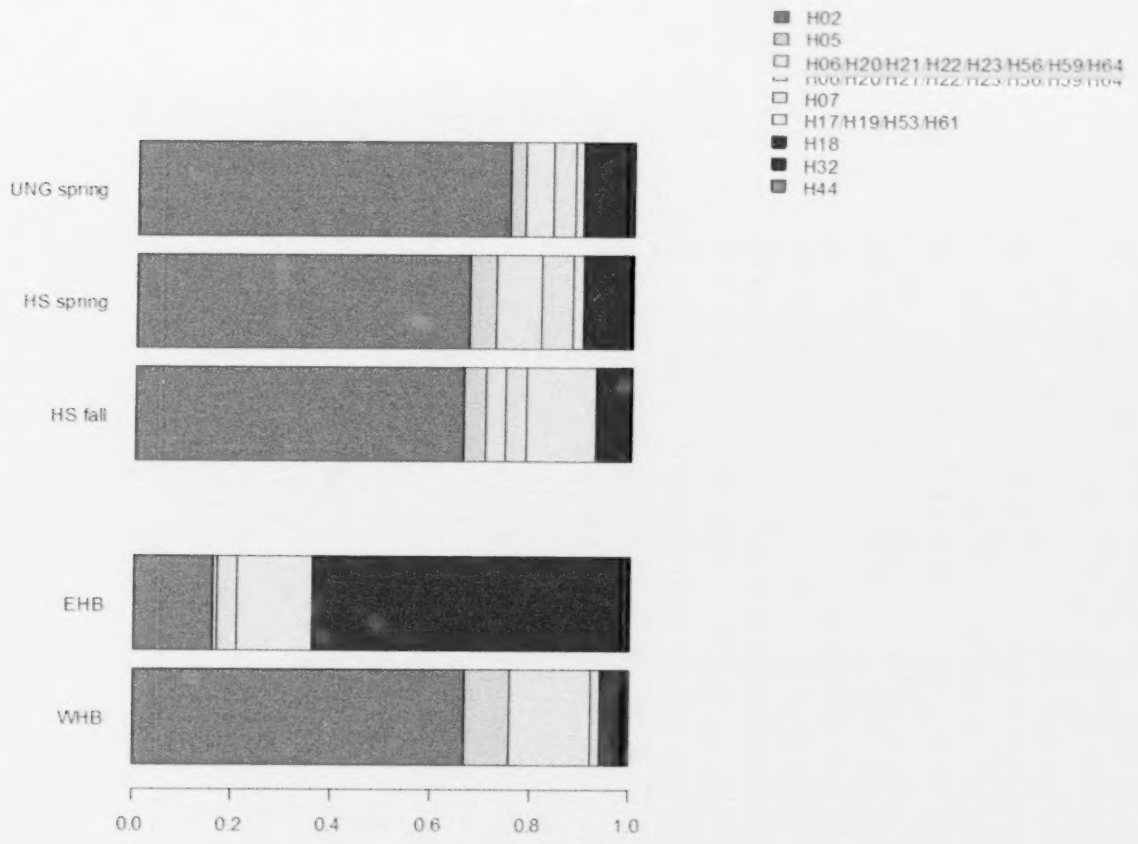

Figure 2. Frequency plot of haplotypes in source areas (bottom, EHB and WHB), and in mixed hunt areas (top). UNG spring, HS spring and HS fall are stated for Ungava spring harvest and Hudson Strait spring and fall harvests respectively. Colour legend shows haplotypes or groups of haplotypes.

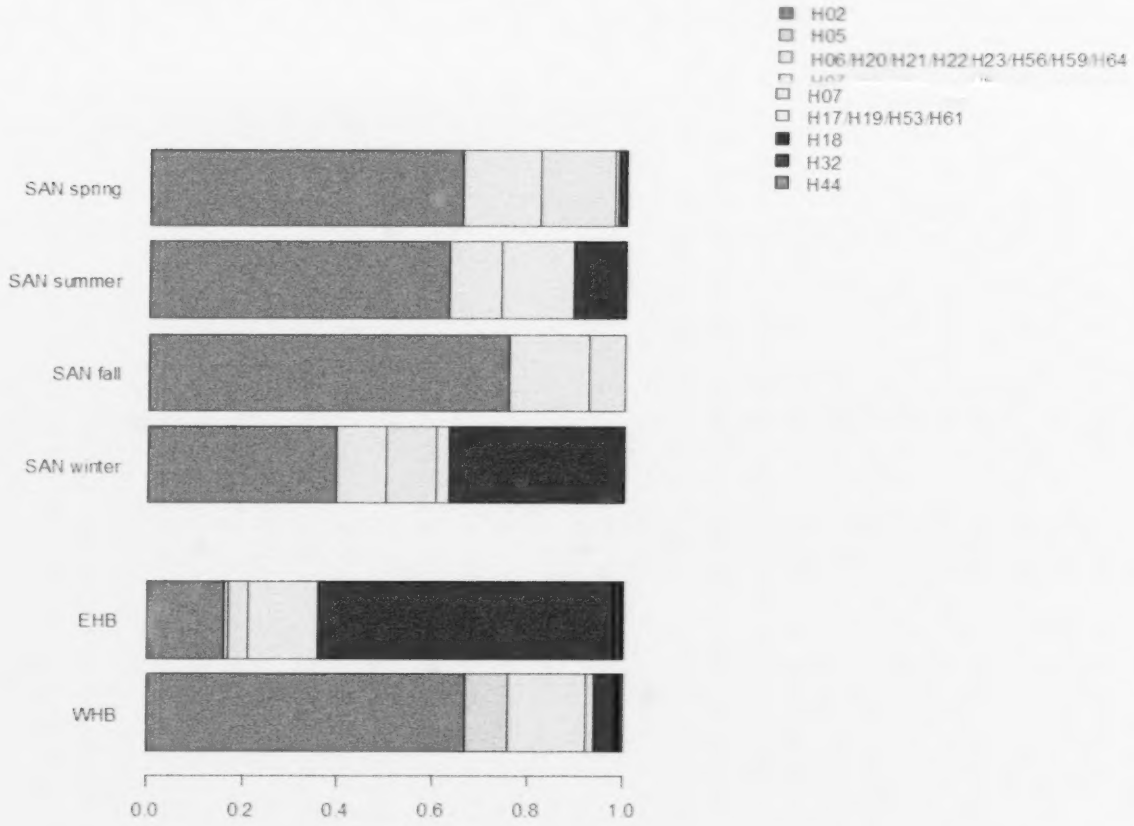

Figure 3. Frequency plot of haplotypes in source areas (bottom, EHB and WHB), and in the Sanikiluaq harvest at different seasons (top). Spring cut-off date is July 14 inclusively. Colour legend shows haplotypes or groups of haplotypes.